

FIG. 1A

Gene #	Intensity in EB 1	Intensity in EB 2	PM > MM in EB 1	PM > MM in EB 2	Induced Ratio	EST #	Accession #	EST?	SAGE?
1	1450	-36.7	0.85	0.35		Hsa.140	M87789 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
2	1450	107	1	0.7	14	Hsa.1534	J00231 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
3	1220	-30.9	0.95	0.45		Hsa.20518	R85690 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
4	1070	86.4	1	0.7	12	Hsa.8219	R46753 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
5	1010	155	0.95	0.7	6	Hsa.2820	Z31695 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
6	1010	53.4	1	0.67	19	Hsa.41163	U06088 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
7	864	46.4	1	0.81	19	Hsa.2836	R71870 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
8	862	148	0.9	0.9	6	Hsa.2551	X57348 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
9	788	137	0.85	0.7	6	Hsa.41123	J00277 gene 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
10	714	139	1	0.95	5	Hsa.13765	X55740 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
11	695	-4.82	1	0.62		Hsa.224	U03106 gene 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
12	645	98.6	0.9	0.8	7	Hsa.8966	X80200 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
13	599	-3.31	1	0.42		Hsa.224	U03106 gene 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
14	582	45.8	0.85	0.55	13	Hsa.1556	L13738 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
15	572	10.5	0.85	0.6	54	Hsa.9103	T67406 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
16	569	46.4	0.95	0.52	12	Hsa.3081	H20434 3' UTR 1	<input type="checkbox"/>	<input type="checkbox"/>
17	538	-99.1	0.93	0.47		Hsa.936	Z20656 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
18	515	25.5	0.95	0.5	20	Hsa.866	M21389 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
19	480	48.1	0.95	0.85	10	Hsa.36025	H28050 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
20	473	31.7	0.9	0.7	15	Hsa.1464	M35878 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
21	463	6.03	0.9	0.4		Hsa.1971	T51913 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
22	445	-9.41	0.94	0.47		Hsa.3011	X63380 gene 1	<input type="checkbox"/>	<input type="checkbox"/>

TO FIG. 1B

FIG. 1B

TO FIG. 1A

23	437	-6.03	0.9	0.5	Hsa.21756	R94967 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
24	385	32.8	0.95	0.55	12 Hsa.1069	T41265 3' UTR 1	<input type="checkbox"/>	<input type="checkbox"/>
25	383	61.2	0.8	0.65	6 Hsa.32222	R69448 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
26	383	21.9	1	0.75	17 Hsa.2611	R59199 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
27	376	10.5	0.94	0.59	36 Hsa.620	M27138 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
28	364	61.1	0.9	0.6	6 Hsa.401	X82166 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
29	353	-34.4	0.85	0.5	Hsa.936	Z20656 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
30	341	-42.5	0.95	0.48	Hsa.3064	X05615 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
31	331	21.1	0.81	0.52	16 Hsa.243	U01147 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
32	329	54	1	0.94	6 Hsa.1432	M64347 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
33	313	55.6	0.95	0.8	6 Hsa.32445	R71505 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
34	293	13.3	0.9	0.55	22 Hsa.3348	X15880 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
35	291	18.7	0.9	0.7	16 Hsa.2000	L16242 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
36	288	-18.3	0.9	0.45	Hsa.8468	H19201 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
37	287	17	0.9	0.62	17 Hsa.169	U02388 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
38	276	40.7	1	0.78	7 Hsa.41094	L18920 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
39	275	37.4	0.9	0.9	7 Hsa.2054	X70340 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
40	269	38.1	0.95	0.8	7 Hsa.21901	R49565 3' UTR 1	<input type="checkbox"/>	<input type="checkbox"/>
41	252	-30.5	0.76	0.48	Hsa.1876	X54156 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
42	250	48.2	0.9	0.55	5 Hsa.2827	Z11502 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
43	247	25.5	1	0.69	10 Hsa.2835	X07696 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>

FIG. 1C

Gene Description	Induced
IG GAMMA-1 CHAIN C REGION (HUMAN);	
Human Ig gamma3 heavy chain disease OMM protein mRNA.	
274912 MYELIN TRANSCRIPTION FACTOR 1 (Homo sapiens)	
152524 CYCLIN-DEPENDENT KINASE INHIBITOR 1 (Homo sapiens)	
H.sapiens mRNA for 43 kDa inositol polyphosphate 5-phosphatase.	
Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.	
155730 KERATIN, TYPE I CYTOSKELETAL 17 (HUMAN);.	
H.sapiens mRNA (clone 9112), kinase related protein.	
c-Ha-ras1 proto-oncogene, complete coding sequence, Human (genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3, 4, 6]).	
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).	
Human wild-type p53 activated fragment-1 (WAF1) mRNA, complete cds.	
H.sapiens MLN62 mRNA.	
Human wild-type p53 activated fragment-1 (WAF1) mRNA, complete cds.	
Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	
81780 COMPLEMENT C4 PRECURSOR (Homo sapiens)	
172486 clone, mRNA for tuberlin, or TSC2 gene.	
Homo sapiens of cardiac alpha-myosin heavy chain gene.	
KERATIN, TYPE II CYTOSKELETAL 5 (HUMAN);contains MSR1 repetitive element ;.	
182000 FK506-BINDING PROTEIN PRECURSOR (Mus musculus)	
Human insulin-like growth factor-binding protein-3 gene, complete cds, clone HL1006d.	
72466 ALPHA CRYSTALLIN B CHAIN (HUMAN).	
Homo sapiens mRNA for serum response factor-related protein, RSRFR2.	

TO FIG. 1D

FIG. 1D

TO FIG. 1C

198656 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (Homo sapiens)
62461 SMALL NUCLEAR RIBONUCLEOPROTEIN Particle N (SNRPN), contains MSR1 repetitive element,.
155335 INTEGRIN ALPHA-3 (Homo sapiens)
41792 TUBULIN BETA-2 CHAIN (HUMAN);.
Human estradiol 17 beta-dehydrogenase gene, complete cds.
H.sapiens mRNA for cystathionine-beta-synthase.
Homo sapiens of cardiac alpha-myosin heavy chain gene.
Human mRNA for thyroglobulin.
Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds.
Human novel growth factor receptor mRNA, 3' cds.
142899 DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (Plasmodium falciparum)
Human mRNA for collagen VI alpha-1 C-terminal globular domain.
Homo sapiens sodium channel type I, beta subunit (SCN1B) mRNA, complete cds.
50887 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDSA (Mus musculus)
Human cytochrome P450 4F2 (CYP4F2) mRNA, complete cds.
Human MAGE-2 gene exons 1-4, complete cds.
H.sapiens mRNA for transforming growth factor alpha.
38251 H.sapiens HSJ1 mRNA.
p53
H.sapiens mRNA for intestine-specific annexin.
KERATIN, TYPE I CYTOSKELETAL 15 (HUMAN); contains MER20 repetitive element ;.

FIG. 1E

Gene #	Intensity in EB 1	Intensity in EB 2	PM > MM in EB 1	PM > MM in EB 2	Induced Ratio	EST #	Accession #	EST?	SAGE?
44	245	26.2	0.8	0.55	9	Hsa.35663	H24346 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
45	245	19.6	0.9	0.5	12	Hsa.3189	U17280 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
46	239	47.6	0.9	1	5	Hsa.1915	L06419 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
47	232	32.8	0.85	0.5	7	Hsa.33725	H04238 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
48	225	-53.5	0.85	0.4		Hsa.693	L31409 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
49	222	18.7	0.94	0.71	12	Hsa.2835	X07696 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
50	218	-0.125	1	0.38		Hsa.2072	Y00406 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
51	217	-28.8	0.9	0.43		Hsa.1159	R85613 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
52	215	-13.5	0.82	0.71		Hsa.19576	T98002 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
53	212	-22.4	0.81	0.38		Hsa.407	M95167 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
54	210	39.5	1	0.8	5	Hsa.31500	R62945 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
55	204	-2.31	0.86	0.43		Hsa.2625	Z18951 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
56	199	8.4	0.85	0.4		Hsa.3344	M74509 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
57	199	32	0.85	0.5	6	Hsa.3893	R42765 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
58	198	15.2	0.86	0.62	13	Hsa.2112	L07597 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
59	194	11.6	0.92	0.33	17	Hsa.1382	U06643 gene 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
60	192	18.1	0.9	0.7	11	Hsa.2208	M67454 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
61	190	-12.6	0.9	0.45		Hsa.2729	V00511 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
62	189	-6.86	0.91	0.45		Hsa.2947	X54936 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
63	183	-20.9	1	0.5		Hsa.2947	X54936 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
64	182	20.9	0.94	0.76	9	Hsa.1870	M79463 gene 1	<input type="checkbox"/>	<input type="checkbox"/>

TO FIG. 1F

FIG. 1F

TO FIG. 1E

65	180	27.7	0.9	0.6	6Hsa.36694	D25217 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
66	178	-77.8	0.89	0.22	Hsa.772	M38451 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
67	178	-39.7	0.9	0.38	Hsa.2402	L36069 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
68	176	-249	0.85	0.35	Hsa.967	M33388 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
69	175	-4.32	0.95	0.45	Hsa.837	M13755 gene 1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
70	165	20.7	1	0.76	8Hsa.37262	R84974 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
71	165	30.1	0.95	0.7	5Hsa.27577	R48578 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
72	165	31.1	0.9	0.65	5Hsa.25777	R62459 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
73	163	25.6	0.8	0.7	6Hsa.35954	H26960 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
74	161	-10.4	0.9	0.5	Hsa.1842	M94547 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
75	157	8.9	0.95	0.6	Hsa.218	T64470 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
76	154	26.3	0.76	0.62	6Hsa.19553	T97948 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
77	147	6.01	0.95	0.65	Hsa.1387	U14631 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
78	141	15.1	0.85	0.7	9Hsa.2823	L05072 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
79	141	20	0.86	0.79	7Hsa.2208	M67454 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
80	141	3.08	0.95	0.65	Hsa.955	M32011 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
81	140	10.1	1	0.48	14Hsa.3279	U28249 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
82	136	7.45	0.95	0.71	Hsa.9537	U28369 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
83	132	6.17	0.81	0.48	Hsa.1846	M96980 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
84	119	-8.34	0.88	0.76	Hsa.36766	H40980 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
85	118	-6.81	0.8	0.6	Hsa.1221	T60155 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
86	117	12.3	0.9	0.6	10Hsa.2826	X07876 gene 1	<input type="checkbox"/>	<input type="checkbox"/>

TO FIG. 1H

FIG. 1H

TO FIG. 1G

Human mRNA (KIAA0027) for ORF, partial cds.
Human placenta-specific growth hormone mRNA, complete cds.
Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds.
Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
INTERFERON-INDUCED 17 KD/ 15 KD PROTEIN (HUMAN)
180447 FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (Homo sapiens)
153585 EBNA-2 NUCLEAR PROTEIN (Epstein-barr virus)
36678 TROPONIN C, ISOFORM 2 (Balanus nubilis)
182125 HDL-BINDING PROTEIN
HUMMLC2At; Homo sapiens: 593 base-pairs
80486 LIVER CARBOXYLESTERASE PRECURSOR (HUMAN);.
121916 NEUTRAL CALPONIN, SMOOTH MUSCLE (Sus scrofa)
Human 11 beta-hydroxysteroid dehydrogenase type II mRNA, complete cds.
Homo sapiens interferon regulatory factor 1 gene, complete cds.
Human Fas antigen (fas) mRNA, complete cds.
NEUTROPHIL OXIDASE FACTOR (p67 PHOX) (HUMAN)
Human 11kd protein mRNA, complete cds.
Human semaphorin V mRNA, complete cds.
MYELIN TRANSCRIPTION FACTOR 1 (HUMAN);.
175991 NEURONAL CALCIUM SENSOR 1 (Rattus norvegicus)
81422 HUMAN SMOOTH MUSCLE ALPHA-ACTIN (AORTIC TYPE)
Human mRNA for irp protein (int-1 related protein).

FIG. 1 I

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Induced Ratio	EST #	Accession #	EST?	SAGE?
87	117	1.9	0.92	0.5		Hsa.2208	M67454 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
88	107	-21.3	0.8	0.45		Hsa.1881	M14083 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
89	107	-0.81	0.8	0.55		Hsa.22529	R37128 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
90	106	0.0333	1	0.5		Hsa.10171	R70008 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
91	105	8.36	0.85	0.7		Hsa.2325	U14747 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
92	105	-6.04	0.9	0.38		Hsa.2980	X77737 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
93	104	14.7	0.9	0.7	7	Hsa.2131	L25541 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
94	103	-168	0.87	0.47		Hsa.967	M33388 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
95	89	-5.05	0.9	0.6		Hsa.1497	M75126	<input type="checkbox"/>	<input type="checkbox"/>
96	85.9	6.79	0.81	0.57		Hsa.2013	Z12020 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
97	84.6	11.9	0.9	0.65	7	Hsa.101	D12620 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
98	82.8	2.73	0.95	0.5		Hsa.1984	J05200 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
99	81.5	11.1	0.85	0.65	7	Hsa.27854	R51856 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
100	79.9	-0.934	0.9	0.45		Hsa.20474	R01072 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>

FIG. 1J

Accession	Gene Description	Induced
Human Fas antigen (fas) mRNA, complete cds.		
Human beta-migrating plasminogen activator inhibitor 1 mRNA, 3' end.		
26063 COMPLEMENT C4 PRECURSOR (Homo sapiens)		
142450 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (Rattus norvegicus)		
Human visinin-like peptide 1 homolog mRNA, complete cds.		
H. sapiens mRNA for red cell anion exchanger (EPB3, AE1, Band 3) 3' non-coding region.		
Human laminin S B3 chain (LAMB3) mRNA, complete cds		
Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.		
Human hexokinase 1 (HK1) mRNA, complete cds.		
Human mRNA for the MDM2 gene.		
Human mRNA for cytochrome P-450LTBV.		
RYANODINE RECEPTOR, SKELETAL MUSCLE (HUMAN);		
39052 POTASSIUM CHANNEL PROTEIN EAG (Drosophila melanogaster)		
124416 SERINE THREONINE-PROTEIN KINASE COT-1 (Neurospora crassa)		

FIG. 2A

Gene #	Intensity in EB 1	Intensity in EB 1	PM > MM in EB 1	PM > MM in EB 1	Ratio	Repressed	EST #	Accession #	EST?	SAGE?
1	400	2750	0.95	1	6.9	Hsa.1137	T57686	3' UTR 1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
2	323	2600	0.75	1	8.04	Hsa.10770	T76971	3' UTR 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
3	411	2300	1	1	5.59	Hsa.1047	R84411	3' UTR 1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
4	261	2010	0.75	0.85	7.7	Hsa.2715	H77597	3' UTR 1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
5	156	1970	0.95	1	12.7	Hsa.14842	T90759	3' UTR 2a	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
6	303	1770	1	1	5.83	Hsa.18397	R81812	3' UTR 2a	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
7	209	1580	0.85	1	7.57	Hsa.1311	R91912	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
8	311	1570	0.95	1	5.05	Hsa.1205	R08183	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
9	245	1460	0.95	1	5.95	Hsa.2806	X77956	gene 1	<input type="checkbox"/>	<input type="checkbox"/>
10	253	1450	0.75	0.95	5.75	Hsa.11673	H23544	3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
11	246	1410	0.9	1	5.73	Hsa.1190	T74556	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
12	62	1350	0.9	1	21.8	Hsa.1505	M12623	gene 1	<input type="checkbox"/>	<input type="checkbox"/>
13	201	1170	0.8	1	5.84	Hsa.1896	J04173	gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
14	178	1110	0.9	1	6.23	Hsa.122	D14696	gene 1	<input type="checkbox"/>	<input type="checkbox"/>
15	176	1100	0.9	1	6.24	Hsa.17649	T87527	3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
16	183	1060	0.9	1	5.8	Hsa.1013	T61661	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
17	102	1030	0.7	0.95	10.1	Hsa.1401	R02151	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
18	120	1020	0.9	1	8.48	Hsa.18401	R23889	3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
19	96.4	999	0.85	1	10.4	Hsa.1676	H73758	3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
20	146	876	0.85	1	5.99	Hsa.1617	D43950	gene 1	<input type="checkbox"/>	<input type="checkbox"/>
21	3.17	867	0.5	0.95		Hsa.115	D14657	gene 1	<input type="checkbox"/>	<input type="checkbox"/>

TO FIG. 2B

FIG. 2B

TO FIG. 2A

22	154	804	0.7	0.95	5.22	Hsa.12893	H49652 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
23	105	632	0.95	1	6.04	Hsa.1043	M29065 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
24	64.5	602	0.75	0.8	9.34	Hsa.448	H09351 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
25	61.4	556	0.6	1	9.05	Hsa.6472	T56604 3' UTR 2a	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
26	48.7	525	0.7	1	10.8	Hsa.1778	J04977 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
27	26.4	495	0.65	0.9	18.8	Hsa.2965	Y00705 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
28	37.3	491	0.75	0.95	13.2	Hsa.1422	M13450 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
29	93.9	487	0.85	1	5.19	Hsa.1046	H29485 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
30	93.6	486	0.85	0.95	5.2	Hsa.3037	X74104 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
31	57.1	468	0.7	0.85	8.19	Hsa.10011	R06239 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
32	84.5	456	0.85	0.95	5.4	Hsa.347	D16111 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
33	66	444	0.71	1	6.73	Hsa.9937	T94834 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
34	54.8	423	0.76	0.86	7.72	Hsa.3253	U14603 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
35	26.7	414	0.8	1	15.5	Hsa.1786	L25941 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
36	48.4	403	0.8	1	8.31	Hsa.14831	H29320 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
37	45.8	400	0.8	0.85	8.74	Hsa.1606	X64330 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
38	62	395	0.9	0.95	6.37	Hsa.116	D14658 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
39	62.4	391	0.86	0.86	6.27	Hsa.3318	H65116 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
40	4.31	364	0.55	0.95		Hsa.13508	R37660 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
41	66.9	351	0.8	1	5.25	Hsa.2959	X74330 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
42	12.1	327	0.52	0.9	27	Hsa.1343	M13665 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
43	44.4	313	0.59	0.88	7.05	Hsa.2459	U10116 gene 1	<input type="checkbox"/>	<input type="checkbox"/>

FIG. 2C

Gene ID	Gene Description	Repressed
79398	TUBULIN ALPHA-1 CHAIN (HUMAN).	
113739	H.sapiens mRNA for metallothionein (HUMAN);.	
194660	SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEINS B AND B' (HUMAN);.	
214162	H.sapiens mRNA for metallothionein (HUMAN);.	
111435	TUBULIN ALPHA-1 CHAIN (Gallus gallus)	
	HUMAN mRNA FOR ADENOCARCINOMA-ASSOCIATED ANTIGEN (KSA), or GA733-2	
196105	PLACENTAL CALCIUM-BINDING PROTEIN (HUMAN);.	
127228	HEAT SHOCK PROTEIN, CHAPERONIN 10, or GroES; MITOCHONDRIAL ;.	
	H.sapiens Id1 mRNA.	
51894	GTP-BINDING NUCLEAR PROTEIN RAN (Homo sapiens)	
84680	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);.	
	Human non-histone chromosomal protein HMG-17 mRNA, complete cds.	
	PHOSPHOGLYCERATE MUTASE, BRAIN FORM (HUMAN).	
	Human mRNA (KIAA0108) for ORF (complete cds) and HepG2 mRNA identical sequence.	
115413	HEAT SHOCK PROTEIN HSP 84 (Mus musculus).	
78161	PROFILIN I (HUMAN)	
124693	RAT mRNA for PROTEASOME SUBUNIT RC10-II, or HUMAN PROTEASOME SUBUNIT HSC10-II.	
131036	TRANSFERRIN RECEPTOR PROTEIN (Homo sapiens)	
214923	PSORIASIS-ASSOCIATED FATTY ACID BINDING PROTEIN HOMOLOG (HUMAN);.	
	Human mRNA (KIAA0098) for ORF (human counterpart of mouse chaperonin containing TCP-1 gene), partial cds.	
	Human mRNA for ORF(KIAA0101), complete cds.	

TO FIG. 2D

FIG. 2D

TO FIG. 2C

274422	ATPASE INHIBITOR, MITOCHONDRIAL (BOVIN).
	Human hnRNP A2 protein mRNA.
46019	MCM3 HOMOLOG (HUMAN);.
73143	TUBULIN BETA-1 CHAIN (Haliotis discus)
	Human Ku autoimmune antigen gene, complete cds.
	Homo sapiens pstI mRNA for pancreatic secretory inhibitor (expressed in neoplastic tissue).
	Human esterase D mRNA, 3'end.
49970	LUPUS LA PROTEIN (HUMAN);.
	H.sapiens mRNA for TRAP beta subunit.
125446	TRANSCRIPTION INITIATION FACTOR TFIID (Homo sapiens)
	Human mRNA for human homologue of rat phosphatidylethanolamine binding protein, complete cds.
120041	HLA-DR ASSOC. PROTEIN I, P31 (also called Ii, In, M1, Dr gamma, XM 1) (Homo sapiens)
	Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence.
	Homo sapiens integral nuclear envelope inner membrane protein (LBR) gene, complete cds.
52626	HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION (Saccharomyces cerevisiae)
	H.sapiens mRNA for ATP-citrate lyase.
	Human mRNA for ORF (KIAA0102), complete cds.
238612	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1 or BSC2) mRNA, complete cds.
26573	STATHMIN (Homo sapiens)
	H.sapiens mRNA for DNA primase (subunit p48).
	Human c-myb mRNA, 3'end.
	Human superoxide dismutase (SOD3 or EC-SOD) gene, complete cds.

FIG. 2E

Gene #	Intensity in EB 1	Intensity in EB	PM > MM in EB 1	PM > MM in EB	Ratio	Repressed EST #	Accession #	EST?	SAGE?
44	47.1	303	0.75	1	6.44	Hsa.1511	V00530 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
45	52.4	299	0.8	0.95	5.7	Hsa.1067	J04543 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
46	50.1	296	0.75	1	5.91	Hsa.1877	M88108 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
47	55.1	294	0.71	0.9	5.33	Hsa.421	D16294 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
48	38.8	290	0.7	0.95	7.48	Hsa.1583	D42084 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
49	-49.3	287	0.62	0.86		Hsa.1625	H59259 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
50	54.3	280	0.76	1	5.16	Hsa.3075	X78627 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
51	43.1	271	0.7	0.95	6.3	Hsa.18494	T93518 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
52	19.9	264	0.55	0.85	13.3	Hsa.1573	D42041 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
53	46.5	262	0.65	0.94	5.64	Hsa.2490	D21262 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
54	22.1	261	0.67	0.9	11.8	Hsa.1595	L32866 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
55	26.1	253	0.76	0.95	9.67	Hsa.1816	T91855 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
56	10.2	251	0.65	0.8	24.6	Hsa.1490	R56440 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
57	29.9	250	0.65	0.95	8.34	Hsa.9856	R60195 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
58	10.4	248	0.65	1	23.9	Hsa.150	L10678 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
59	40.2	245	0.95	0.85	6.09	Hsa.7048	R56401 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
60	6.69	242	0.57	0.95		Hsa.1315	D13639 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
61	41.2	234	0.65	0.95	5.7	Hsa.21993	R12588 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
62	43.4	234	0.65	0.8	5.38	Hsa.970	M77836 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
63	22.2	211	0.8	0.95	9.51	Hsa.17935	H01943 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
64	26.6	206	0.57	0.95	7.73	Hsa.10122	T52362 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
65	27.1	195	0.8	0.85	7.2	Hsa.654	L33930 gene 1	<input type="checkbox"/>	<input type="checkbox"/>

TO FIG. 2F

FIG. 2F

TO FIG. 2E

66	27.2	195	0.7	0.9	7.18	Hsa.10779	X87212 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
67	17	190	0.7	0.95	11.2	Hsa.1815	L31801 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
68	-4.22	189	0.6	0.8		Hsa.3091	T49870 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
69	28.1	187	0.5	0.8	6.65	Hsa.462	U09564 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
70	5.53	186	0.8	0.9		Hsa.42520	H64001 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
71	21.6	175	0.6	0.8	8.09	Hsa.1460	M20867 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
72	31.8	173	0.6	0.85	5.45	Hsa.14771	T70251 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
73	20.3	171	0.76	0.86	8.41	Hsa.9868	T50501 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
74	31.5	169	0.7	1	5.36	Hsa.2892	X76029 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
75	17.7	168	0.67	0.9	9.49	Hsa.1361	M14219 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
76	14.5	166	0.75	1	11.5	Hsa.12976	X74987 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
77	27	164	0.55	0.9	6.06	Hsa.2485	D14694 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
78	-8.48	159	0.37	0.84		Hsa.234	L19183 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
79	30.9	157	0.8	0.9	5.09	Hsa.1242	T55008 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
80	15.8	147	0.7	0.95	9.33	Hsa.25724	R46716 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
81	28.6	145	0.7	0.85	5.07	Hsa.38007	R88418 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
82	28.5	145	0.65	0.9	5.09	Hsa.1780	R09502 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
83	23	145	0.7	0.95	6.29	Hsa.1615	D43948 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
84	20.8	142	0.85	0.95	6.82	Hsa.13795	H00297 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
85	7.23	141	0.55	0.8		Hsa.1665	L23959 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
86	24.6	140	0.67	1	5.67	Hsa.928	M22538 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>

FIG. 2G

Gene Description	Repressed
Human mRNA encoding IMP:pyrophosphate phosphoribosyltransferase E.C. 2.4.2.8.	
Human synexin mRNA, complete cds.	
Human p62 mRNA, complete cds.	
Human mRNA for mitochondrial 3-oxoacyl-CoA thiolase, complete cds.	
Human mRNA (KIAA0094) for ORF (yeast methionine aminopeptidase-related), partial cds.	
204299 REPLICATION PROTEIN A 14 KD SUBUNIT (HUMAN);	
H.sapiens mRNA for translin.	
117708 MYOSIN HEAVY CHAIN, CLONE 203 (Hydra attenuata)	
Human mRNA (KIAA0088) for ORF (alpha-glucosidase-related), partial cds.	
Human mRNA (KIAA0035) for ORF (rat 140kd nucleolar phosphoprotein homologue), partial cds.	
Human effector cell protease receptor-1 (EPR-1) gene, partial cds.	
112020 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (HUMAN);	
40874 TUBULIN GAMMA CHAIN (HUMAN);	
42829 EUKARYOTIC INITIATION FACTOR 4B (Homo sapiens)	
PROFILIN II (HUMAN);	
40753 RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN, RanGAP (Homo sapiens)	
Human mRNA for ORF (KIAK0002), or HUMAN D-TYPE CYCLIN complete cds.	
128385 HAMSTER RNA FOR CYCLIN B2 (mesocricetus auratus)	
PYRROLINE-5-CARBOXYLATE REDUCTASE (HUMAN);	
150169 EUKARYOTIC INITIATION FACTOR 4E (Homo sapiens)	
72050 NUCLEOTIDE-SENSITIVE CHLORIDE CHANNEL (Canis familiaris), or HUMAN CHLORIDE CHANNEL REGULATORY PROTEIN mRNA	

TO FIG. 2H

FIG. 2H

TO FIG. 2G

Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region.
H.sapiens mRNA for cathepsin C (dipeptidyl peptidase I).
Homo sapiens monocarboxylate transporter 1 (SLC16A1) mRNA, complete cds.
68690 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (HUMAN).
Human serine kinase (SRPK1) mRNA, complete cds.
209484 CD9 ANTIGEN (Bos taurus), or HUMAN T245 PROTEIN
Human glutamate dehydrogenase (GDH) mRNA, complete cds.
109334 NEGATIVE REGULATOR OF MITOSIS (Emericella nidulans)
77138 EUKARYOTIC INITIATION FACTOR 1A (Sac cerevisiae), or HUMAN PROTEIN SYNTHESIS FACTOR 4C(eIF-4C)
H.sapiens mRNA for neuromedin U.
Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.
H.sapiens mRNA for 2'-5' oligoadenylate binding protein.
Human mRNA (K1AA0024) for ORF (putative human counterpart of chinese hamster phosphatidylserine synthase gene), complete cds.
Human MAC30 mRNA, 3' end.
74167 APOLIPOPROTEIN A-II PRECURSOR (HUMAN).
36504 GTPASE ACTIVATING PROTEIN ROTUND (Drosophila melanogaster)
166353 CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (Homo sapiens)
127707 LAMININ BETA-1 CHAIN PRECURSOR (HUMAN);.
Human mRNA (K1AA0097) for ORF (novel protein), complete cds.
149556 O-ANTIGEN POLYMERASE (Shigella flexneri)
Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds.
NADH-UBIQUINONE DEHYDROGENASE 24 KD SUBUNIT PRECURSOR (HUMAN);.

FIG. 2I

Gene #	Intensity in EB 1	Intensity in EB 2	PM > MM in EB 1	PM > MM in EB 2	Ratio	EST #	Accession #	EST?	SAGE?
87	27.1	139	0.8	0.9	5.14	Hsa.1811	M37510 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
88	17.2	137	0.4	0.9	7.95	Hsa.6633	R61359 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
89	20.8	136	0.4	0.9	6.55	Hsa.13172	T73788 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
90	19.7	135	0.65	0.85	6.85	Hsa.1423	J04102 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
91	18.1	134	0.57	0.9	7.41	Hsa.13967	T66747 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
92	19.2	134	0.7	1	6.96	Hsa.1245	M21154 gene 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
93	7.16	132	0.71	1		Hsa.13508	R37660 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
94	-0.0563	130	0.65	0.85		Hsa.28663	H10045 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
95	6.27	129	0.55	0.95		Hsa.1200	D38553 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
96	8.89	128	0.67	0.9		Hsa.2070	J04088 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
97	1.42	124	0.7	0.9		Hsa.45678	H88978 3' UTR 2a	<input type="checkbox"/>	<input type="checkbox"/>
98	13.2	123	0.45	0.9	9.27	Hsa.18077	H02009 3' UTR 2a	<input checked="" type="checkbox"/>	<input type="checkbox"/>
99	12.3	121	0.62	0.95	9.84	Hsa.1219	M16827 gene 1	<input type="checkbox"/>	<input type="checkbox"/>
100	10.9	119	0.5	0.9	11	Hsa.1952	T96666 3' UTR 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>

FIG. 2J

Gene Description	Repressed
Human methylmalonyl CoA mutase (MUT) gene, exon 13.	
37866 BASIGIN PRECURSOR (Gallus gallus)	
84443 GA BINDING PROTEIN BETA-1 CHAIN (Homo sapiens)	
Human erythroblastosis virus oncogene homolog 2 (ets-2) mRNA, complete cds.	
53193 26S PROTEASE REGULATORY SUBUNIT 6 (Homo sapiens)	
S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (HUMAN);.	
26573 STATHMIN (Homo sapiens)	
46827 VAV ONCOGENE (Homo sapiens)	
Human mRNA (KIAA0074) for ORF (yeast C728 protein-related), partial cds.	
Human DNA topoisomerase II gene (top2), gene 1	
Homo sapiens cDNA clone 253186 3'	
151010 EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (Homo sapiens)	
Human medium-chain acyl-CoA dehydrogenase (ACADM) mRNA, complete cds.	
121357 A49436 CD11=CYCLIN-DEPENDENT KINASE INTERACTOR 1 - ;.	